

2

SEQUENCE LISTING

<110> Tsukahara, Kappei
Tsuchiya, Mamiko
Jigami, Yoshifumi
Nakayama, Kenichi
Umemura, Mariko
Okamoto, Michiyo

<120> METHOD OF SCREENING FOR COMPOUNDS THAT
INHIBIT THE ENZYMATIC ACTIVITY OF GWT1 GENE PRODUCT

<130> 082368-004400US

<140> 10/536,935

<141>

<150> PCT/JP03/14909

<151> 2003-11-21

<150> JP 2002-339418

<151> 2002-11-22

<160> 18

<170> FastSEQ for Windows Version 4.0

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<211> 1497

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

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gag	gac	ttt	gtt	aca	ggg	ctc	aat	ggc	ggt	tct	ata	aca	gaa	att	aac		96
Glu	Asp	Phe	Val	Thr	Gly	Leu	Asn	Gly	Gly	Ser	Ile	Thr	Glu	Ile	Asn		
20								25					30				

gca	gtt	aca	tca	att	gct	ttt	gtt	act	tac	ata	tca	tgg	aac	tta	ttt		144
Ala	Val	Thr	Ser	Ile	Ala	Leu	Val	Thr	Tyr	Ile	Ser	Trp	Asn	Leu	Leu		
35								40				45					

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tat	gct	agt	gaa	cca	tac	ctt	cta	aac	acg	cta	ata	ctg	tta	cct	tgt		288
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85	90	95	
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aat cca ata tac aat aaa aaa atg att aca cag cgg ttc caa cta Asn Pro Ile Tyr Asn Lys Lys Met Ile Thr Gln Arg Phe Gln Leu 115	120	125	384
gaa aaa aag ccg tat att act gcg tat cgt ggt ggg atg ctt att ctg Glu Lys Lys Pro Tyr Ile Thr Ala Tyr Arg Gly Gly Met Leu Ile Leu 130	135	140	432
act gct att gcc atc ttg gct gta gat ttt cca att ttc cca agg agg Thr Ala Ile Ala Ile Leu Ala Val Asp Phe Pro Ile Phe Pro Arg Arg 145	150	155	480
ttt gcc aag gtg gaa act tgg ggg aca tcc ctg atg gat ctt ggt gta Phe Ala Lys Val Glu Thr Trp Gly Thr Ser Leu Met Asp Leu Gly Val 165	170	175	528
gga tca ttc gtt ttc agt aac ggt att gtt tct tct agg gca ctg ttg Gly Ser Phe Val Phe Ser Asn Gly Ile Val Ser Ser Arg Ala Leu Leu 180	185	190	576
aaa aac cta agc ttg a'ag agt aaa ccc agc ttc tta aaa aat gca ttt Lys Asn Leu Ser Leu Lys Ser Lys Pro Ser Phe Leu Lys Asn Ala Phe 195	200	205	624
aat gcc tta aaa tca gga gga act cta ttg ttc cta gga ttg ctg agg Asn Ala Leu Lys Ser Gly Gly Thr Leu Leu Phe Leu Gly Leu Leu Arg 210	215	220	672
ttg ttt ttt gta aaa aat ttg gaa tat caa gaa cat gtc aca gaa tat Leu Phe Phe Val Lys Asn Leu Glu Tyr Gln Glu His Val Thr Glu Tyr 225	230	235	720
ggg gtt cat tgg aat ttt ttc acc cta tca ttg ttg cca ctt gta Gly Val His Trp Asn Phe Phe Ile Thr Leu Ser Leu Leu Pro Leu Val 245	250	255	768
ttg acc ttt att gat ccc gtc aca aga atg gtt cca cgc tgc tca att Leu Thr Phe Ile Asp Pro Val Thr Arg Met Val Pro Arg Cys Ser Ile 260	265	270	816
gca ata ttc att tca tgc att tat gaa tgg cta ctt tta aag gac gat Ala Ile Phe Ile Ser Cys Ile Tyr Glu Trp Leu Leu Leu Lys Asp Asp 275	280	285	864
cgc act tta aac ttt tta att ttg gct gat aga aat tgt ttc ttc agt Arg Thr Leu Asn Phe Leu Ile Leu Ala Asp Arg Asn Cys Phe Phe Ser 290	295	300	912
gct aat aga gaa ggc atc ttc tca ttt cta ggt tat tgc tcg att ttt Ala Asn Arg Glu Gly Ile Phe Ser Phe Leu Gly Tyr Cys Ser Ile Phe 305	310	315	960
ctt tgg ggc caa aac acg gga ttt tac ttg ttg gga aat aaa cca act Leu Trp Gly Gln Asn Thr Gly Phe Tyr Leu Leu Gly Asn Lys Pro Thr 325	330	335	1008

tta aac aat ctt tat aag cct tct acg caa gac gta gtt gca gca tca Leu Asn Asn Leu Tyr Lys Pro Ser Thr Gln Asp Val Val Ala Ala Ser 340 345 350	1056
aag aag tct tcg act tgg gac tat tgg act tca gta acc cca tta agt Lys Lys Ser Ser Thr Trp Asp Tyr Trp Thr Ser Val Thr Pro Leu Ser 355 360 365	1104
ggc ctc tgt ata tgg agt aca att ttt ctt gtt atc agc cag ttg gtt Gly Leu Cys Ile Trp Ser Thr Ile Phe Leu Val Ile Ser Gln Leu Val 370 375 380	1152
ttt caa tac cat cct tat agt gtt tca aga agg ttt gct aac tta cca Phe Gln Tyr His Pro Tyr Ser Val Ser Arg Arg Phe Ala Asn Leu Pro 385 390 395 400	1200
tat act ttg tgg gtc att act tat aat tta cta ttt ttg act ggg tac Tyr Thr Leu Trp Val Ile Thr Tyr Asn Leu Leu Phe Leu Thr Gly Tyr 405 410 415	1248
tgc ttg act gac aaa att ttc ggt aat tct tcg gaa tat tat aaa gtt Cys Leu Thr Asp Lys Ile Phe Gly Asn Ser Ser Glu Tyr Tyr Lys Val 420 425 430	1296
gcc gaa tgc ttg gaa tca atc aac tcc aat ggg ttg ttt tta ttt ttg Ala Glu Cys Leu Glu Ser Ile Asn Ser Asn Gly Leu Phe Leu Phe Leu 435 440 445	1344
ttg gca aat gtc tct act ggt tta gtc aat atg tct atg gtc acg ata Leu Ala Asn Val Ser Thr Gly Leu Val Asn Met Ser Met Val Thr Ile 450 455 460	1392
gat tct tca ccc tta aaa tca ttc ctg gtt ttg ttg gca tac tgc tca Asp Ser Ser Pro Leu Lys Ser Phe Leu Val Leu Leu Ala Tyr Cys Ser 465 470 475 480	1440
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Lys Asn Ser Asn Leu Met Pro Pro Gly Ile Ser Ser Val Gln Tyr Ile
50 55 60

Ile Asp Phe Ala Leu Asn Trp Val Ala Leu Leu Leu Ser Ile Thr Ile
65 70 75 80

Tyr Ala Ser Glu Pro Tyr Leu Leu Asn Thr Leu Ile Leu Leu Pro Cys
85 90 95

Leu Leu Ala Phe Ile Tyr Gly Lys Phe Thr Ser Ser Lys Pro Ser
100 105 110

Asn Pro Ile Tyr Asn Lys Lys Met Ile Thr Gln Arg Phe Gln Leu
115 120 125

Glu Lys Lys Pro Tyr Ile Thr Ala Tyr Arg Gly Gly Met Leu Ile Leu
130 135 140

Thr Ala Ile Ala Ile Leu Ala Val Asp Phe Pro Ile Phe Pro Arg Arg
145 150 155 160

Phe Ala Lys Val Glu Thr Trp Gly Thr Ser Leu Met Asp Leu Gly Val
165 170 175

Gly Ser Phe Val Phe Ser Asn Gly Ile Val Ser Ser Arg Ala Leu Leu
180 185 190

Lys Asn Leu Ser Leu Lys Ser Lys Pro Ser Phe Leu Lys Asn Ala Phe
195 200 205

Asn Ala Leu Lys Ser Gly Gly Thr Leu Leu Phe Leu Gly Leu Leu Arg
210 215 220

Leu Phe Phe Val Lys Asn Leu Glu Tyr Gln Glu His Val Thr Glu Tyr
225 230 235 240

Gly Val His Trp Asn Phe Phe Ile Thr Leu Ser Leu Leu Pro Leu Val
245 250 255

Leu Thr Phe Ile Asp Pro Val Thr Arg Met Val Pro Arg Cys Ser Ile
260 265 270

Ala Ile Phe Ile Ser Cys Ile Tyr Glu Trp Leu Leu Leu Lys Asp Asp
275 280 285

Arg Thr Leu Asn Phe Leu Ile Leu Ala Asp Arg Asn Cys Phe Phe Ser
290 295 300

Ala Asn Arg Glu Gly Ile Phe Ser Phe Leu Gly Tyr Cys Ser Ile Phe
305 310 315 320

Leu Trp Gly Gln Asn Thr Gly Phe Tyr Leu Leu Gly Asn Lys Pro Thr
325 330 335

Leu Asn Asn Leu Tyr Lys Pro Ser Thr Gln Asp Val Val Ala Ala Ser
340 345 350

Lys Lys Ser Ser Thr Trp Asp Tyr Trp Thr Ser Val Thr Pro Leu Ser
355 360 365

Gly Leu Cys Ile Trp Ser Thr Ile Phe Leu Val Ile Ser Gln Leu Val
 370 375 380
 Phe Gln Tyr His Pro Tyr Ser Val Ser Arg Arg Phe Ala Asn Leu Pro
 385 390 395 400
 Tyr Thr Leu Trp Val Ile Thr Tyr Asn Leu Leu Phe Leu Thr Gly Tyr
 405 410 415
 Cys Leu Thr Asp Lys Ile Phe Gly Asn Ser Ser Glu Tyr Tyr Lys Val
 420 425 430
 Ala Glu Cys Leu Glu Ser Ile Asn Ser Asn Gly Leu Phe Leu Phe Leu
 435 440 445
 Leu Ala Asn Val Ser Thr Gly Leu Val Asn Met Ser Met Val Thr Ile
 450 455 460
 Asp Ser Ser Pro Leu Lys Ser Phe Leu Val Leu Leu Ala Tyr Cys Ser
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 Thr Gly Gly Thr Ile Glu Glu Ile Tyr Ala Val Thr Ser Ile Ala Leu
 20 25 30
 tca tct tat ttg tcc ttt aga ttg ttg aaa aag tct ctt ggt gat tta 144
 Ser Ser Tyr Leu Ser Phe Arg Leu Leu Lys Lys Ser Leu Gly Asp Leu
 35 40 45
 gct ttg att tac gac tac att ctt aat gtg ttg aca att cta gca tcc 192
 Ala Leu Ile Tyr Asp Tyr Ile Leu Asn Val Leu Thr Ile Leu Ala Ser
 50 55 60
 att act gtt tat agc aac agc cct tct tat ttg cat tat ttt att gtt 240
 Ile Thr Val Tyr Ser Asn Ser Pro Ser Tyr Leu His Tyr Phe Ile Val
 65 70 75 80
 att cca tca tta gtt ata tat cta gtg aat tac cat gtt gag aaa cca 288
 Ile Pro Ser Leu Val Ile Tyr Leu Val Asn Tyr His Val Glu Lys Pro
 85 90 95

tct tca ccc cat aga caa aat gat aca aaa gaa gat aaa tcg gac gaa	336		
Ser Ser Pro His Arg Gln Asn Asp Thr Lys Glu Asp Lys Ser Asp Glu			
100	105	110	
cta ttg ccg aga aaa caa ttt ata aca gcc tat cgt tct caa atg ttg	384		
Leu Leu Pro Arg Lys Gln Phe Ile Thr Ala Tyr Arg Ser Gln Met Leu			
115	120	125	
ata att act aat cta gct ata tta gct gtt gat ttt cct att ttc cca	432		
Ile Ile Thr Asn Leu Ala Ile Leu Ala Val Asp Phe Pro Ile Phe Pro			
130	135	140	
aga aga ttt gcc aaa gtg gaa aca tgg ggc acg tca atg atg gat tta	480		
Arg Arg Phe Ala Lys Val Glu Thr Trp Gly Thr Ser Met Met Asp Leu			
145	150	155	160
gga gtt ggg tcg ttt gtg ttc tcc atg ggg ttg gct aat tct cga caa	528		
Gly Val Gly Ser Phe Val Phe Ser Met Gly Leu Ala Asn Ser Arg Gln			
165	170	175	
ttg atc aag aac cac acc gac aac tac aaa ttt agt tgg aag agt tat	576		
Leu Ile Lys Asn His Thr Asp Asn Tyr Lys Phe Ser Trp Lys Ser Tyr			
180	185	190	
ttg aaa aca atc aag cag aac ttt atc aag tca gtg cct ata ctt gtt	624		
Leu Lys Thr Ile Lys Gln Asn Phe Ile Lys Ser Val Pro Ile Leu Val			
195	200	205	
tta gga gct att cgt ttt gtt agt gtt aag caa ttg gac tat cag gaa	672		
Leu Gly Ala Ile Arg Phe Val Ser Val Lys Gln Leu Asp Tyr Gln Glu			
210	215	220	
cac gaa aca gag tat gga atc cat tgg aat ttt ttc ttc aca tta ggg	720		
His Glu Thr Glu Tyr Gly Ile His Trp Asn Phe Phe Thr Leu Gly			
225	230	235	240
ttc ttg cca att gta ttg gga ata tta gac ccg gtg ttg aat ttg gtt	768		
Phe Leu Pro Ile Val Leu Gly Ile Leu Asp Pro Val Leu Asn Leu Val			
245	250	255	
cca cgc ttc ata ata gga att ggt atc tca att gct tat gag gta gcg	816		
Pro Arg Phe Ile Ile Gly Ile Gly Ile Ser Ile Ala Tyr Glu Val Ala			
260	265	270	
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275	280	285	
ctt gaa tct ctc atc acc atg aat aaa gaa ggt att ttt tcg ttt att	912		
Leu Glu Ser Leu Ile Thr Met Asn Lys Glu Gly Ile Phe Ser Phe Ile			
290	295	300	
gga tat ctt tgt att ttt ata att ggt cag tct ttt ggg tca ttt gtt	960		
Gly Tyr Leu Cys Ile Phe Ile Ile Gly Gln Ser Phe Gly Ser Phe Val			
305	310	315	320
tta aca ggc tac aaa aca aag aac aac tta ata acc att agc aaa att	1008		
Leu Thr Gly Tyr Lys Thr Lys Asn Asn Leu Ile Thr Ile Ser Lys Ile			
325	330	335	

cgt att tca aaa aaa caa cac aag aaa gag ctg ctg ctg ttt ttc tca Arg Ile Ser Lys Lys Gln His Lys Lys Glu Leu Leu Leu Phe Phe Ser 340 345 350	1056
gtc gcc act act cag gga tta tat ttg gca tgt atc ttc tat cac tta Val Ala Thr Thr Gln Gly Leu Tyr Leu Ala Cys Ile Phe Tyr His Leu 355 360 365	1104
gct ttc agt ttg ttc atc agc aac tta tca ttc ttg caa cca att tca Ala Phe Ser Leu Phe Ile Ser Asn Leu Ser Phe Leu Gln Pro Ile Ser 370 375 380	1152
aga cga ttg gcc aat ttc ccc tac gtc atg tgg gtc gtt tcg tac aat Arg Arg Leu Ala Asn Phe Pro Tyr Val Met Trp Val Val Ser Tyr Asn 385 390 395 400	1200
gct acg ttt tta tta tgt tat gac tta att gaa aaa ttt atc ccg ggg Ala Thr Phe Leu Leu Cys Tyr Asp Leu Ile Glu Lys Phe Ile Pro Gly 405 410 415	1248
aac ctt act tct act gta ttg gac tct att aat aac aat ggt tta ttt Asn Leu Thr Ser Thr Val Leu Asp Ser Ile Asn Asn Asn Gly Leu Phe 420 425 430	1296
atc ttc ttg gtc agc aat tta tta aca ggg ttt att aac atg tcc atc Ile Phe Leu Val Ser Asn Leu Leu Thr Gly Phe Ile Asn Met Ser Ile 435 440 445	1344
aac act ttg gaa act agc aat aaa atg gca gtg att atc ttg att ggc Asn Thr Leu Glu Thr Ser Asn Lys Met Ala Val Ile Ile Leu Ile Gly 450 455 460	1392
tat agt ctt act ttg aca ttg ctc gcc tta tat ttg gat aag agg aag Tyr Ser Leu Thr Trp Thr Leu Leu Ala Leu Tyr Leu Asp Lys Arg Lys 465 470 475 480	1440
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Ser Ser Tyr Leu Ser Phe Arg Leu Leu Lys Lys Ser Leu Gly Asp Leu 35 40 45
Ala Leu Ile Tyr Asp Tyr Ile Leu Asn Val Leu Thr Ile Leu Ala Ser 50 55 60
Ile Thr Val Tyr Ser Asn Ser Pro Ser Tyr Leu His Tyr Phe Ile Val

65	70	75	80
Ile Pro Ser Leu Val Ile Tyr Leu Val Asn Tyr His Val Glu Lys Pro			
85	90	95	
Ser Ser Pro His Arg Gln Asn Asp Thr Lys Glu Asp Lys Ser Asp Glu			
100	105	110	
Leu Leu Pro Arg Lys Gln Phe Ile Thr Ala Tyr Arg Ser Gln Met Leu			
115	120	125	
Ile Ile Thr Asn Leu Ala Ile Leu Ala Val Asp Phe Pro Ile Phe Pro			
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Arg Arg Phe Ala Lys Val Glu Thr Trp Gly Thr Ser Met Met Asp Leu			
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Gly Val Gly Ser Phe Val Phe Ser Met Gly Leu Ala Asn Ser Arg Gln			
165	170	175	
Leu Ile Lys Asn His Thr Asp Asn Tyr Lys Phe Ser Trp Lys Ser Tyr			
180	185	190	
Leu Lys Thr Ile Lys Gln Asn Phe Ile Lys Ser Val Pro Ile Leu Val			
195	200	205	
Leu Gly Ala Ile Arg Phe Val Ser Val Lys Gln Leu Asp Tyr Gln Glu			
210	215	220	
His Glu Thr Glu Tyr Gly Ile His Trp Asn Phe Phe Phe Thr Leu Gly			
225	230	235	240
Phe Leu Pro Ile Val Leu Gly Ile Leu Asp Pro Val Leu Asn Leu Val			
245	250	255	
Pro Arg Phe Ile Ile Gly Ile Gly Ile Ser Ile Ala Tyr Glu Val Ala			
260	265	270	
Leu Asn Lys Thr Gly Leu Leu Lys Phe Ile Leu Ser Ser Glu Asn Arg			
275	280	285	
Leu Glu Ser Leu Ile Thr Met Asn Lys Glu Gly Ile Phe Ser Phe Ile			
290	295	300	
Gly Tyr Leu Cys Ile Phe Ile Ile Gly Gln Ser Phe Gly Ser Phe Val			
305	310	315	320
Leu Thr Gly Tyr Lys Thr Lys Asn Asn Leu Ile Thr Ile Ser Lys Ile			
325	330	335	
Arg Ile Ser Lys Lys Gln His Lys Lys Glu Leu Leu Leu Phe Phe Ser			
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Val Ala Thr Thr Gln Gly Leu Tyr Leu Ala Cys Ile Phe Tyr His Leu			
355	360	365	
Ala Phe Ser Leu Phe Ile Ser Asn Leu Ser Phe Leu Gln Pro Ile Ser			
370	375	380	
Arg Arg Leu Ala Asn Phe Pro Tyr Val Met Trp Val Val Ser Tyr Asn			

385	390	395	400
Ala Thr Phe Leu Leu Cys Tyr Asp Leu Ile Glu Lys Phe Ile Pro Gly			
405	410	415	
Asn Leu Thr Ser Thr Val Leu Asp Ser Ile Asn Asn Asn Gly Leu Phe			
420	425	430	
Ile Phe Leu Val Ser Asn Leu Leu Thr Gly Phe Ile Asn Met Ser Ile			
435	440	445	
Asn Thr Leu Glu Thr Ser Asn Lys Met Ala Val Ile Ile Leu Ile Gly			
450	455	460	
Tyr Ser Leu Thr Trp Thr Leu Leu Ala Leu Tyr Leu Asp Lys Arg Lys			
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Ile Tyr Ile Lys Leu			
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act ggt ggc aca att gaa gaa att tat gct gta acc agt ata gca tta				96
Thr Gly Gly Thr Ile Glu Glu Ile Tyr Ala Val Thr Ser Ile Ala Leu				
20	25	30		
tca tct tat ttg tcc ttt aga ttg ttg aaa aag tct ctt ggt gat tta				144
Ser Ser Tyr Leu Ser Phe Arg Leu Leu Lys Lys Ser Leu Gly Asp Leu				
35	40	45		
gct ttg att tac gac tac att ctt aat gtg ttg aca att cta gca tcc				192
Ala Leu Ile Tyr Asp Tyr Ile Leu Asn Val Leu Thr Ile Leu Ala Ser				
50	55	60		
att act gtt tat agc aac agc cct tct tat ttg cat tat ttt att gtt				240
Ile Thr Val Tyr Ser Asn Ser Pro Ser Tyr Leu His Tyr Phe Ile Val				
65	70	75	80	
att cca tca tta gtt ata tat cta gtg aat tac cat gtt gag aaa cca				288
Ile Pro Ser Leu Val Ile Tyr Leu Val Asn Tyr His Val Glu Lys Pro				
85	90	95		
tct tca ccc cat aga caa aat gat aca aaa gaa gat aaa tcg gac gaa				336
Ser Ser Pro His Arg Gln Asn Asp Thr Lys Glu Asp Lys Ser Asp Glu				
100	105	110		
cta ttg ccg aga aaa caa ttt ata aca gcc tat cgt tct caa atg ttg				384
Leu Leu Pro Arg Lys Gln Phe Ile Thr Ala Tyr Arg Ser Gln Met Leu				

115	120	125	
ata att act aat cta gct ata tta gct gtt gat ttt cct att ttc cca Ile Ile Thr Asn Leu Ala Ile Leu Ala Val Asp Phe Pro Ile Phe Pro 130	135	140	432
aga aga ttt gcc aaa gtg gaa aca tgg ggc acg tca atg atg gat tta Arg Arg Phe Ala Lys Val Glu Thr Trp Gly Thr Ser Met Met Asp Leu 145	150	155	480
gga gtt ggg tcg ttt gtg ttc tcc atg ggg ttg gct aat tct cga caa Gly Val Gly Ser Phe Val Phe Ser Met Gly Leu Ala Asn Ser Arg Gln 165	170	175	528
ttg atc aag aac cac acc gac aat tac aaa ttt agt tgg aag agt tat Leu Ile Lys Asn His Thr Asp Asn Tyr Lys Phe Ser Trp Lys Ser Tyr 180	185	190	576
ttg aaa aca atc aag cag aac ttt atc aag tca gtg cct ata ctt gtt Leu Lys Thr Ile Lys Gln Asn Phe Ile Lys Ser Val Pro Ile Leu Val 195	200	205	624
tta gga gct att cgt ttt gtt agt gtt aag caa ttg gac tat cag gaa Leu Gly Ala Ile Arg Phe Val Ser Val Lys Gln Leu Asp Tyr Gln Glu 210	215	220	672
cac gaa aca gag tat gga atc cat tgg aat ttt ttc ttc aca tta ggg His Glu Thr Glu Tyr Gly Ile His Trp Asn Phe Phe Thr Leu Gly 225	230	235	720
ttc ttg cca att gta ttg gga ata tta gac ccg gtg ttg aat ttg gtt Phe Leu Pro Ile Val Leu Gly Ile Leu Asp Pro Val Leu Asn Leu Val 245	250	255	768
cca cgc ttc ata ata gga att ggt atc tca att ggt tat gag gta gcg Pro Arg Phe Ile Ile Gly Ile Gly Ile Ser Ile Gly Tyr Glu Val Ala 260	265	270	816
ttg aat aag act ggt ttg ttg aag ttc att ttg agc agc gaa aac aga Leu Asn Lys Thr Gly Leu Leu Lys Phe Ile Leu Ser Ser Glu Asn Arg 275	280	285	864
ctt gaa tct ctc atc gcc atg aat aaa gaa ggt att ttt tcg ttt att Leu Glu Ser Leu Ile Ala Met Asn Lys Glu Gly Ile Phe Ser Phe Ile 290	295	300	912
gga tat ctt tgt att ttt ata att ggt cag tct ttt ggg tca ttt gtt Gly Tyr Leu Cys Ile Phe Ile Ile Gly Gln Ser Phe Gly Ser Phe Val 305	310	315	960
tta aca ggc tac aaa aca aag aac aac tta ata acc att agc aaa att Leu Thr Gly Tyr Lys Thr Lys Asn Asn Leu Ile Thr Ile Ser Lys Ile 325	330	335	1008
cgt att tca aaa aaa caa cac aag aaa gag ctg ctg ctg ttt ttc tca Arg Ile Ser Lys Lys Gln His Lys Lys Glu Leu Leu Leu Phe Phe Ser 340	345	350	1056
gtc gcc act act cag gga tta tat ttg gca tgt atc ttc tat cac tta Val Ala Thr Thr Gln Gly Leu Tyr Leu Ala Cys Ile Phe Tyr His Leu 355	360	365	1104

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aga cga ttg gcc aat ttc ccc tac gtc atg tgg gtc gtt tcg tac aat Arg Arg Leu Ala Asn Phe Pro Tyr Val Met Trp Val Val Ser Tyr Asn 385 390 395 400	1200
gct acg ttt tta tta tgt tat gac tta att gaa aaa ttt atc ccg ggg Ala Thr Phe Leu Leu Cys Tyr Asp Leu Ile Glu Lys Phe Ile Pro Gly 405 410 415	1248
aac ctt act tct act gta ttg gac tct att aat aac aat ggt tta ttt Asn Leu Thr Ser Thr Val Leu Asp Ser Ile Asn Asn Asn Gly Leu Phe 420 425 430	1296
atc ttc ttg gtc agc aat tta tta aca ggg ttt att aac atg tcc atc Ile Phe Leu Val Ser Asn Leu Leu Thr Gly Phe Ile Asn Met Ser Ile 435 440 445	1344
aac act ttg gaa act agc aat aaa atg gca gtg att atc ttg att ggc Asn Thr Leu Glu Thr Ser Asn Lys Met Ala Val Ile Ile Leu Ile Gly 450 455 460	1392
tat agt ctt act tgg aca ttg ctc gcc tta tat ttg gat aag agg aag Tyr Ser Leu Thr Trp Thr Leu Leu Ala Leu Tyr Leu Asp Lys Arg Lys 465 470 475 480	1440
atc tac atc aag ctt tag Ile Tyr Ile Lys Leu 485	1458

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<211> 485
<212> PRT
<213> Candida albicans

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Thr Gly Gly Thr Ile Glu Glu Ile Tyr Ala Val Thr Ser Ile Ala Leu 20 25 30	
Ser Ser Tyr Leu Ser Phe Arg Leu Leu Lys Lys Ser Leu Gly Asp Leu 35 40 45	
Ala Leu Ile Tyr Asp Tyr Ile Leu Asn Val Leu Thr Ile Leu Ala Ser 50 55 60	
Ile Thr Val Tyr Ser Asn Ser Pro Ser Tyr Leu His Tyr Phe Ile Val 65 70 75 80	
Ile Pro Ser Leu Val Ile Tyr Leu Val Asn Tyr His Val Glu Lys Pro 85 90 95	
Ser Ser Pro His Arg Gln Asn Asp Thr Lys Glu Asp Lys Ser Asp Glu 100 105 110	

Leu Leu Pro Arg Lys Gln Phe Ile Thr Ala Tyr Arg Ser Gln Met Leu
115 120 125

Ile Ile Thr Asn Leu Ala Ile Leu Ala Val Asp Phe Pro Ile Phe Pro
130 135 140

Arg Arg Phe Ala Lys Val Glu Thr Trp Gly Thr Ser Met Met Asp Leu
145 150 155 160

Gly Val Gly Ser Phe Val Phe Ser Met Gly Leu Ala Asn Ser Arg Gln
165 170 175

Leu Ile Lys Asn His Thr Asp Asn Tyr Lys Phe Ser Trp Lys Ser Tyr
180 185 190

Leu Lys Thr Ile Lys Gln Asn Phe Ile Lys Ser Val Pro Ile Leu Val
195 200 205

Leu Gly Ala Ile Arg Phe Val Ser Val Lys Gln Leu Asp Tyr Gln Glu
210 215 220

His Glu Thr Glu Tyr Gly Ile His Trp Asn Phe Phe Thr Leu Gly
225 230 235 240

Phe Leu Pro Ile Val Leu Gly Ile Leu Asp Pro Val Leu Asn Leu Val
245 250 255

Pro Arg Phe Ile Ile Gly Ile Gly Ile Ser Ile Gly Tyr Glu Val Ala
260 265 270

Leu Asn Lys Thr Gly Leu Leu Lys Phe Ile Leu Ser Ser Glu Asn Arg
275 280 285

Leu Glu Ser Leu Ile Ala Met Asn Lys Glu Gly Ile Phe Ser Phe Ile
290 295 300

Gly Tyr Leu Cys Ile Phe Ile Ile Gly Gln Ser Phe Gly Ser Phe Val
305 310 315 320

Leu Thr Gly Tyr Lys Thr Lys Asn Asn Leu Ile Thr Ile Ser Lys Ile
325 330 335

Arg Ile Ser Lys Lys Gln His Lys Lys Glu Leu Leu Phe Phe Ser
340 345 350

Val Ala Thr Thr Gln Gly Leu Tyr Leu Ala Cys Ile Phe Tyr His Leu
355 360 365

Ala Phe Ser Leu Phe Ile Ser Asn Leu Ser Phe Leu Gln Pro Ile Ser
370 375 380

Arg Arg Leu Ala Asn Phe Pro Tyr Val Met Trp Val Val Ser Tyr Asn
385 390 395 400

Ala Thr Phe Leu Leu Cys Tyr Asp Leu Ile Glu Lys Phe Ile Pro Gly
405 410 415

Asn Leu Thr Ser Thr Val Leu Asp Ser Ile Asn Asn Asn Gly Leu Phe
420 425 430

Ile Phe Leu Val Ser Asn Leu Leu Thr Gly Phe Ile Asn Met Ser Ile

435

440

445

Asn Thr Leu Glu Thr Ser Asn Lys Met Ala Val Ile Ile Leu Ile Gly
 450 455 460

Tyr Ser Leu Thr Trp Thr Leu Leu Ala Leu Tyr Leu Asp Lys Arg Lys
 465 470 475 480

Ile Tyr Ile Lys Leu
 485

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 <211> 1380
 <212> DNA
 <213> Schizosaccharomyces pombe

<220>
 <221> CDS
 <222> (1)..(1380)

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 Met Ser Tyr Lys Leu Glu Lys Glu Ala Phe Val Ser Asn Leu Thr Gly
 1 5 10 15
 tca agt tcc att gag aca tgt ggc ttg tta tta ata gga att gct tgc 96
 Ser Ser Ser Ile Glu Thr Cys Gly Leu Leu Leu Ile Gly Ile Ala Cys
 20 25 30
 aac gtt ttg tgg gta aac atg act gcg aga aac atc tta ccc aaa ggg 144
 Asn Val Leu Trp Val Asn Met Thr Ala Arg Asn Ile Leu Pro Lys Gly
 35 40 45
 aat ctt ggg ttt ctt gtt gag ttt ttc atc ttt tgc tta att cca tta 192
 Asn Leu Gly Phe Leu Val Glu Phe Phe Ile Phe Cys Leu Ile Pro Leu
 50 55 60
 ttt gtc att tac gtt tca tcg aaa gtt ggc gtt ttc act ctt tgc ata 240
 Phe Val Ile Tyr Val Ser Ser Lys Val Gly Val Phe Thr Leu Cys Ile
 65 70 75 80
 gcc tct ttt ttg cct tcc ttc gtc ctt cat gtt ata agt cca att aat 288
 Ala Ser Phe Leu Pro Ser Phe Val Leu His Val Ile Ser Pro Ile Asn
 85 90 95
 tgg gat gtg ctg aga aga aaa cct ggt tgt ctt act aaa aaa aat 336
 Trp Asp Val Leu Arg Arg Lys Pro Gly Cys Cys Leu Thr Lys Lys Asn
 100 105 110
 gaa aat act ttt gat cga cga att gct gga gtc aca ttt tat cgt tct 384
 Glu Asn Thr Phe Asp Arg Arg Ile Ala Gly Val Thr Phe Tyr Arg Ser
 115 120 125
 caa atg atg ttg gtt act gtc act tgc atc ctg gcc gtt gac ttt acc 432
 Gln Met Met Leu Val Thr Val Thr Cys Ile Leu Ala Val Asp Phe Thr
 130 135 140
 ctt ttc ccg agg aga tat gcc aaa gtt gaa acc tgg gga aca tca ctg 480
 Leu Phe Pro Arg Arg Tyr Ala Lys Val Glu Thr Trp Gly Thr Ser Leu

145	150	155	160	
atg gat ctt ggt gtt gga tct ttc atg ttt tct tca ggt act gtg gct Met Asp Leu Gly Val Gly Ser Phe Met Phe Ser Ser Gly Thr Val Ala				528
165	170		175	
gga cgg aaa aat gac att aaa aaa cca aat gcg ttt aaa aat gta ttg Gly Arg Lys Asn Asp Ile Lys Pro Asn Ala Phe Lys Asn Val Leu				576
180	185		190	
tgg aat tct ttc atc ctt ttg att tta gga ttt gcg cgc atg ttt tta Trp Asn Ser Phe Ile Leu Leu Ile Leu Gly Phe Ala Arg Met Phe Leu				624
195	200		205	
acg aaa agc atc aat tac caa gaa cat gta agc gaa tat ggc atg cat Thr Lys Ser Ile Asn Tyr Gln Glu His Val Ser Glu Tyr Gly Met His				672
210	215		220	
tgg aac ttt ttc acc cta ggt ttc atg gct ctt ggc gta ttt ttt Trp Asn Phe Phe Thr Leu Gly Phe Met Ala Leu Gly Val Phe Phe				720
225	230		235	
240				
ttt cgt cgt tct tta aaa aaa gtc tcc tat ttt aat tta gca acc ttc Phe Arg Arg Ser Leu Lys Lys Val Ser Tyr Phe Asn Leu Ala Thr Phe				768
245	250		255	
att act ctt ctt cat cat tgt ttg ctt gtt tta acc cct ttc caa aaa Ile Thr Leu Leu His His Cys Leu Leu Val Leu Thr Pro Phe Gln Lys				816
260	265		270	
tgg gca cta tcc gcc ccc aga aca aat att ttg gct cag aat aga gag Trp Ala Leu Ser Ala Pro Arg Thr Asn Ile Leu Ala Gln Asn Arg Glu				864
275	280		285	
ggt att gct tct ccc gga tac att gct att tac ttt tat gga atg Gly Ile Ala Ser Leu Pro Gly Tyr Ile Ala Ile Tyr Phe Tyr Gly Met				912
290	295		300	
tat acc ggt agt gta gtt ttg gct gat cga cct cta atg tat act aga Tyr Thr Gly Ser Val Val Leu Ala Asp Arg Pro Leu Met Tyr Thr Arg				960
305	310		315	
320				
gct gag tcg tgg aag cgc ttt caa cgt cta tta ttc ccg cta tgc att Ala Glu Ser Trp Lys Arg Phe Gln Arg Leu Leu Phe Pro Leu Cys Ile				1008
325	330		335	
ttg tta gtg ttg tat ctt gtg tct aac ttt ttg tca gtt ggt gtt tct Leu Leu Val Leu Tyr Leu Val Ser Asn Phe Leu Ser Val Gly Val Ser				1056
340	345		350	
cgc cga ctt gct aat acg cct tat gtt gcg aat gtt gcc ttt atc aat Arg Arg Leu Ala Asn Thr Pro Tyr Val Ala Asn Val Ala Phe Ile Asn				1104
355	360		365	
atg ttt ttt ctt act ata tac ata ctt att gat gcc tat tta ttc cca Met Phe Phe Leu Thr Ile Tyr Ile Leu Ile Asp Ala Tyr Leu Phe Pro				1152
370	375		380	
tct tct gtg cca tat gga agt cgc gtc ccc aaa ctg ctt gaa gat gcc Ser Ser Val Pro Tyr Gly Ser Arg Val Pro Lys Leu Leu Glu Asp Ala				1200
385	390		395	
400				

aat aat aat ggc ttg ttg gtg ttt ttg att gct aac gtt tta aca gga	1248
Asn Asn Asn Gly Leu Leu Val Phe Leu Ile Ala Asn Val Leu Thr Gly	
405 410 415	
gta gtt aat tta tcg ttc gac acc ctt cat tct agc aat gca aaa ggc	1296
Val Val Asn Leu Ser Phe Asp Thr Leu His Ser Ser Asn Ala Lys Gly	
420 425 430	
ttg aca atc atg act atg tat ctt ttt att att tgc tat atg gca cat	1344
Leu Thr Ile Met Thr Met Tyr Leu Phe Ile Ile Cys Tyr Met Ala His	
435 440 445	
tgg ctt gct caa cac gga att cgt ttt cgc ctt tag	1380
Trp Leu Ala Gln His Gly Ile Arg Phe Arg Leu	
450 455	
<210> 8	
<211> 459	
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<213> Schizosaccharomyces pombe	
<400> 8	
Met Ser Tyr Lys Leu Glu Lys Glu Ala Phe Val Ser Asn Leu Thr Gly	1248
1 5 10 15	
Ser Ser Ser Ile Glu Thr Cys Gly Leu Leu Leu Ile Gly Ile Ala Cys	1296
20 25 30	
Asn Val Leu Trp Val Asn Met Thr Ala Arg Asn Ile Leu Pro Lys Gly	1344
35 40 45	
Asn Leu Gly Phe Leu Val Glu Phe Phe Ile Phe Cys Leu Ile Pro Leu	1380
50 55 60	
Phe Val Ile Tyr Val Ser Ser Lys Val Gly Val Phe Thr Leu Cys Ile	1428
65 70 75 80	
Ala Ser Phe Leu Pro Ser Phe Val Leu His Val Ile Ser Pro Ile Asn	1468
85 90 95	
Trp Asp Val Leu Arg Arg Lys Pro Gly Cys Cys Leu Thr Lys Asn	1508
100 105 110	
Glu Asn Thr Phe Asp Arg Arg Ile Ala Gly Val Thr Phe Tyr Arg Ser	1548
115 120 125	
Gln Met Met Leu Val Thr Val Thr Cys Ile Leu Ala Val Asp Phe Thr	1588
130 135 140	
Leu Phe Pro Arg Arg Tyr Ala Lys Val Glu Thr Trp Gly Thr Ser Leu	1628
145 150 155 160	
Met Asp Leu Gly Val Gly Ser Phe Met Phe Ser Ser Gly Thr Val Ala	1668
165 170 175	
Gly Arg Lys Asn Asp Ile Lys Lys Pro Asn Ala Phe Lys Asn Val Leu	1708
180 185 190	
Trp Asn Ser Phe Ile Leu Ile Leu Gly Phe Ala Arg Met Phe Leu	1748

195	200	205
Thr Lys Ser Ile Asn Tyr Gln Glu His Val Ser Glu Tyr Gly Met His		
210	215	220
Trp Asn Phe Phe Phe Thr Leu Gly Phe Met Ala Leu Gly Val Phe Phe		
225	230	235
Phe Arg Arg Ser Leu Lys Lys Val Ser Tyr Phe Asn Leu Ala Thr Phe		
245	250	255
Ile Thr Leu Leu His His Cys Leu Leu Val Leu Thr Pro Phe Gln Lys		
260	265	270
Trp Ala Leu Ser Ala Pro Arg Thr Asn Ile Leu Ala Gln Asn Arg Glu		
275	280	285
Gly Ile Ala Ser Leu Pro Gly Tyr Ile Ala Ile Tyr Phe Tyr Gly Met		
290	295	300
Tyr Thr Gly Ser Val Val Leu Ala Asp Arg Pro Leu Met Tyr Thr Arg		
305	310	315
320		
Ala Glu Ser Trp Lys Arg Phe Gln Arg Leu Leu Phe Pro Leu Cys Ile		
325	330	335
Leu Leu Val Leu Tyr Leu Val Ser Asn Phe Leu Ser Val Gly Val Ser		
340	345	350
Arg Arg Leu Ala Asn Thr Pro Tyr Val Ala Asn Val Ala Phe Ile Asn		
355	360	365
Met Phe Phe Leu Thr Ile Tyr Ile Leu Ile Asp Ala Tyr Leu Phe Pro		
370	375	380
Ser Ser Val Pro Tyr Gly Ser Arg Val Pro Lys Leu Leu Glu Asp Ala		
385	390	395
400		
Asn Asn Asn Gly Leu Leu Val Phe Leu Ile Ala Asn Val Leu Thr Gly		
405	410	415
Val Val Asn Leu Ser Phe Asp Thr Leu His Ser Ser Asn Ala Lys Gly		
420	425	430
Leu Thr Ile Met Thr Met Tyr Leu Phe Ile Ile Cys Tyr Met Ala His		
435	440	445
Trp Leu Ala Gln His Gly Ile Arg Phe Arg Leu		
450	455	

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 <211> 1576
 <212> DNA
 <213> Aspergillus fumigatus

<220>
 <221> CDS
 <222> (31)..(1536)

<400> 9

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aaa gag gcc ttt gtc tca ggt ctt gca gga gga agc atc ctg gaa atc Lys Glu Ala Phe Val Ser Gly Leu Ala Gly Gly Ser Ile Leu Glu Ile 10 15 20	102
aac gcc gtc acc ttg gtt gct tcg gta tcc gtt ttt ctg tgg tca att Asn Ala Val Thr Leu Val Ala Ser Val Ser Val Phe Leu Trp Ser Ile 25 30 35 40	150
cta caa tct cgc cta tcc ttt ttc aca ccc tac agc gcc gct gcc ctt Leu Gln Ser Arg Leu Ser Phe Thr Pro Tyr Ser Ala Ala Ala Leu 45 50 55	198
ctc gtt gat ttc ctg ctc aat gta cta gct atc ttg ttc gca acc act Leu Val Asp Phe Leu Leu Asn Val Leu Ala Ile Leu Phe Ala Thr Thr 60 65 70	246
tta tac tct tcg gcg cct ctt ctc aat ctc ctt cta ata tct ccc Leu Tyr Ser Ser Ala Pro Leu Leu Asn Leu Leu Ile Ser Pro 75 80 85	294
gct ctg ctg ata ctc ctc tct acg aaa cgt cct cgg acc ccc gtc aaa Ala Leu Leu Ile Leu Ser Thr Lys Arg Pro Arg Thr Pro Val Lys 90 95 100	342
gcg aaa cct cct cgc cag tcc gct aga gct ggg aaa gat gac tcg aaa Ala Lys Pro Pro Arg Gln Ser Ala Arg Ala Gly Lys Asp Asp Ser Lys 105 110 115 120	390
cat gcg aca gcc ttg cca gag tct cta ccc att cat cca ttt ctc acg His Ala Thr Ala Leu Pro Glu Ser Leu Pro Ile His Pro Phe Leu Thr 125 130 135	438
aca tat cgc gcc gcc atg atg gtt atc acg tcg atc gct atc ttg gct Thr Tyr Arg Ala Ala Met Met Val Ile Thr Cys Ile Ala Ile Leu Ala 140 145 150	486
gtg gat ttt cgc att ttt cct cgc cga ttc gcc aag gta gaa aac tgg Val Asp Phe Arg Ile Phe Pro Arg Arg Phe Ala Lys Val Glu Asn Trp 155 160 165	534
ggt aca tca ctc atg gat ctg ggc gtt gga tcg ttt gtc ttt tcg ggc Gly Thr Ser Leu Met Asp Leu Gly Val Gly Ser Phe Val Phe Ser Gly 170 175 180	582
gga gta gta tcc gct cgc tca cta ctc aag agc agg acc aat ggc tct Gly Val Val Ser Ala Arg Ser Leu Leu Lys Ser Arg Thr Asn Gly Ser 185 190 195 200	630
aaa agg ttg cct ctt gcc aag agg ttg att gcg tcg acg cga cac tct Lys Arg Leu Pro Leu Ala Lys Arg Leu Ile Ala Ser Thr Arg His Ser 205 210 215	678
att cct ctg ctc gtc ctc ggc ctg att cgg cta tac agc gtc aaa ggc Ile Pro Leu Leu Val Leu Gly Leu Ile Arg Leu Tyr Ser Val Lys Gly 220 225 230	726
ttg gac tat gcg gag cac gtc acc gag tac ggc gta cat tgg aac ttc	774

Leu	Asp	Tyr	Ala	Glu	His	Val	Thr	Glu	Tyr	Gly	Val	His	Trp	Asn	Phe	
235																245
ttc ttt aca ttg ggt ctt ttg cct ccg ttc gtg gag gtc ttc gac gcc															822	
Phe	Phe	Thr	Leu	Gly	Leu	Leu	Pro	Pro	Phe	Val	Glu	Val	Phe	Asp	Ala	
250																260
ttg gct acg atc att ccg tca tac gag gtt ctc tcc gtg ggg atc gcc															870	
Leu	Ala	Thr	Ile	Ile	Pro	Ser	Tyr	Glu	Val	Leu	Ser	Val	Gly	Ile	Ala	
265																280
gtc ttg tat caa gtt gcc cta gag tca aca gac ttg aaa agc tac atc															918	
Val	Leu	Tyr	Gln	Val	Ala	Leu	Glu	Ser	Thr	Asp	Leu	Lys	Ser	Tyr	Ile	
285																295
ctc gtc tcc cct cgt ggg cca agc tta ctg tcc aag aat cgt gaa ggc															966	
Leu	Val	Ser	Pro	Arg	Gly	Pro	Ser	Leu	Leu	Ser	Lys	Asn	Arg	Glu	Gly	
300																310
gtc ttc tcc ttc tca ggt tat ctc gcg att ttt ctt gct ggt cgt gcg															1014	
Val	Phe	Ser	Phe	Ser	Gly	Tyr	Leu	Ala	Ile	Phe	Leu	Ala	Gly	Arg	Ala	
315																325
atc ggc att cgg ata atc cct cgc gga act tct ttc tca aga agc cca															1062	
Ile	Gly	Ile	Arg	Ile	Ile	Pro	Arg	Gly	Thr	Ser	Phe	Ser	Arg	Ser	Pro	
330																340
gaa cag gcc agg aga cgg gtc ctg atc agc ctt ggc gtg caa gcg tta															1110	
Glu	Gln	Ala	Arg	Arg	Val	Leu	Ile	Ser	Leu	Gly	Val	Gln	Ala	Leu		
345																360
gtg tgg acc act ctt ttt gtg ttg aac tcc act tat gcg atg gga tac															1158	
Val	Trp	Thr	Leu	Phe	Val	Leu	Asn	Ser	Thr	Tyr	Ala	Met	Gly	Tyr		
365																375
gga gct aat atc cct gtc tcc cgc cgc ctc gct aac atg ccc tat gtc															1206	
Gly	Ala	Asn	Ile	Pro	Val	Ser	Arg	Arg	Leu	Ala	Asn	Met	Pro	Tyr	Val	
380																390
ctt tgg gtt tcg gcg ttc aac acc gcg caa ctg ttt gtg ttc tgc ctg															1254	
Leu	Trp	Val	Ser	Ala	Phe	Asn	Thr	Ala	Gln	Leu	Phe	Val	Phe	Cys	Leu	
395																405
atc gaa aca ctc tgc ttt cct gca gtt cat cgg aca acg act caa gag															1302	
Ile	Glu	Thr	Leu	Cys	Phe	Pro	Ala	Val	His	Arg	Thr	Thr	Thr	Gln	Glu	
410																420
agc gaa tct gag cga gtc gat ttt gct acg agc cga atc atg tcg gcc															1350	
Ser	Glu	Ser	Glu	Arg	Val	Asp	Phe	Ala	Thr	Ser	Arg	Ile	Met	Ser	Ala	
425																440
ttc aat aag aac agt ctc gcg atc ttt ctt ttg gcc aat ctt ctg act															1398	
Phe	Asn	Lys	Asn	Ser	Leu	Ala	Ile	Phe	Leu	Leu	Ala	Asn	Leu	Leu	Thr	
445																455
gga gct gtg aat ctg agc atc tcc aca att gat gct aat aca gcg cag															1446	
Gly	Ala	Val	Asn	Leu	Ser	Ile	Ser	Thr	Ile	Asp	Ala	Asn	Thr	Ala	Gln	
460																470
gcc atc gct gtt ctc att gga tat tca tcc att atc aca ggg gtt gct															1494	
Ala	Ile	Ala	Val	Leu	Ile	Gly	Tyr	Ser	Ser	Ile	Ile	Thr	Gly	Val	Ala	

475	480	485	
cta gca ttg cat cat gcc aat atc aaa gta ctt cct ttc tag			
Leu Ala Leu His His Ala Asn Ile Lys Val Leu Pro Phe			
490	495	500	
ggtatttacg agcaatttgtt ggtgtgttga agatata tag			1576
<210> 10			
<211> 501			
<212> PRT			
<213> Aspergillus fumigatus			
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1	5	10	15
Ala Gly Gly Ser Ile Leu Glu Ile Asn Ala Val Thr Leu Val Ala Ser			
20	25	30	
Val Ser Val Phe Leu Trp Ser Ile Leu Gln Ser Arg Leu Ser Phe Phe			
35	40	45	
Thr Pro Tyr Ser Ala Ala Leu Leu Val Asp Phe Leu Leu Asn Val			
50	55	60	
Leu Ala Ile Leu Phe Ala Thr Leu Tyr Ser Ser Ala Pro Leu Leu			
65	70	75	80
Leu Asn Leu Leu Leu Ile Ser Pro Ala Leu Leu Ile Leu Leu Ser Thr			
85	90	95	
Lys Arg Pro Arg Thr Pro Val Lys Ala Lys Pro Pro Arg Gln Ser Ala			
100	105	110	
Arg Ala Gly Lys Asp Asp Ser Lys His Ala Thr Ala Leu Pro Glu Ser			
115	120	125	
Leu Pro Ile His Pro Phe Leu Thr Thr Tyr Arg Ala Ala Met Met Val			
130	135	140	
Ile Thr Cys Ile Ala Ile Leu Ala Val Asp Phe Arg Ile Phe Pro Arg			
145	150	155	160
Arg Phe Ala Lys Val Glu Asn Trp Gly Thr Ser Leu Met Asp Leu Gly			
165	170	175	
Val Gly Ser Phe Val Phe Ser Gly Gly Val Val Ser Ala Arg Ser Leu			
180	185	190	
Leu Lys Ser Arg Thr Asn Gly Ser Lys Arg Leu Pro Leu Ala Lys Arg			
195	200	205	
Leu Ile Ala Ser Thr Arg His Ser Ile Pro Leu Leu Val Leu Gly Leu			
210	215	220	
Ile Arg Leu Tyr Ser Val Lys Gly Leu Asp Tyr Ala Glu His Val Thr			
225	230	235	240

Glu Tyr Gly Val His Trp Asn Phe Phe Phe Thr Leu Gly Leu Leu Pro
 245 250 255
 Pro Phe Val Glu Val Phe Asp Ala Leu Ala Thr Ile Ile Pro Ser Tyr
 260 265 270
 Glu Val Leu Ser Val Gly Ile Ala Val Leu Tyr Gln Val Ala Leu Glu
 275 280 285
 Ser Thr Asp Leu Lys Ser Tyr Ile Leu Val Ser Pro Arg Gly Pro Ser
 290 295 300
 Leu Leu Ser Lys Asn Arg Glu Gly Val Phe Ser Phe Ser Gly Tyr Leu
 305 310 315 320
 Ala Ile Phe Leu Ala Gly Arg Ala Ile Gly Ile Arg Ile Ile Pro Arg
 325 330 335
 Gly Thr Ser Phe Ser Arg Ser Pro Glu Gln Ala Arg Arg Arg Val Leu
 340 345 350
 Ile Ser Leu Gly Val Gln Ala Leu Val Trp Thr Thr Leu Phe Val Leu
 355 360 365
 Asn Ser Thr Tyr Ala Met Gly Tyr Gly Ala Asn Ile Pro Val Ser Arg
 370 375 380
 Arg Leu Ala Asn Met Pro Tyr Val Leu Trp Val Ser Ala Phe Asn Thr
 385 390 395 400
 Ala Gln Leu Phe Val Phe Cys Leu Ile Glu Thr Leu Cys Phe Pro Ala
 405 410 415
 Val His Arg Thr Thr Thr Gln Glu Ser Glu Ser Glu Arg Val Asp Phe
 420 425 430
 Ala Thr Ser Arg Ile Met Ser Ala Phe Asn Lys Asn Ser Leu Ala Ile
 435 440 445
 Phe Leu Leu Ala Asn Leu Leu Thr Gly Ala Val Asn Leu Ser Ile Ser
 450 455 460
 Thr Ile Asp Ala Asn Thr Ala Gln Ala Ile Ala Val Leu Ile Gly Tyr
 465 470 475 480
 Ser Ser Ile Ile Thr Gly Val Ala Leu Ala Leu His His Ala Asn Ile
 485 490 495
 Lys Val Leu Pro Phe
 500

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 <212> DNA
 <213> Aspergillus fumigatus

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 <222> (122)..(198)

<220>
<221> CDS
<222> (26)..(121)

<220>
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Glu Ala Phe Val Ser Gly Leu Ala Gly Ser Ile Leu Glu Ile Asn
10 15 20 25

gcc gtc acc ttg gtt gct tcg gttcgtgtta ctatcttatt gtggctactt 151
Ala Val Thr Leu Val Ala Ser
30

cgcttacatt gtttctcgac taaccgagtc tctttgcgttcaatcgtt gta tcc gtt 207
Val Ser Val
35

ttt ctg tgg tca att cta caa tct cgc cta tcc ttt ttc aca ccc tac 255
Phe Leu Trp Ser Ile Leu Gln Ser Arg Leu Ser Phe Phe Thr Pro Tyr
40 45 50

agc gcc gct gcc ctt ctc gtt gat ttc ctg ctc aat gta cta gct atc 303
Ser Ala Ala Leu Leu Val Asp Phe Leu Leu Asn Val Leu Ala Ile
55 60 65

ttg ttc gca acc act tta tac tct tcg gcg cct ctt ctc aat ctc 351
Leu Phe Ala Thr Thr Leu Tyr Ser Ser Ala Pro Leu Leu Asn Leu
70 75 80

ctt cta ata tct ccc gct ctg ctg ata ctc ctc tct acg aaa cgt cct 399
Leu Leu Ile Ser Pro Ala Leu Leu Ile Leu Ser Thr Lys Arg Pro
85 90 95

cg acc ccc gtc aaa gcg aaa cct cct cgc cag tcc gct aga gct ggg 447
Arg Thr Pro Val Lys Ala Lys Pro Pro Arg Gln Ser Ala Arg Ala Gly
100 105 110 115

aaa gat gac tcg aaa cat gcg aca gcc ttg cca gag tct cta ccc att 495
Lys Asp Asp Ser Lys His Ala Thr Ala Leu Pro Glu Ser Leu Pro Ile
120 125 130

cat cca ttt ctc acg aca tat cgc gcc atg atg gtt atc acg tgc 543
His Pro Phe Leu Thr Thr Tyr Arg Ala Ala Met Met Val Ile Thr Cys
135 140 145

atc gct atc ttg gct gtg gat ttt cct cgc cga ttc gcc 591
Ile Ala Ile Leu Ala Val Asp Phe Arg Ile Phe Pro Arg Arg Phe Ala
150 155 160

aag gta gaa aac tgg ggt aca tca ctc atg gat ctg ggc gtt gga tcg 639
Lys Val Glu Asn Trp Gly Thr Ser Leu Met Asp Leu Gly Val Gly Ser
165 170 175

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agg acc aat ggc tct aaa agg ttg cct ctt gcc aag agg ttg att gcg Arg Thr Asn Gly Ser Lys Arg Leu Pro Leu Ala Lys Arg Leu Ile Ala 200 205 210	735
tcg acg cga cac tct att cct ctg ctc gtc ctc ggc ctg att cgg cta Ser Thr Arg His Ser Ile Pro Leu Leu Val Leu Gly Leu Ile Arg Leu 215 220 225	783
tac agc gtc aaa ggc ttg gac tat gcg gag cac gtc acc gag tac ggc Tyr Ser Val Lys Gly Leu Asp Tyr Ala Glu His Val Thr Glu Tyr Gly 230 235 240	831
gta cat tgg aac ttc ttc ttt aca ttg ggt ctt ttg cct ccg ttc gtg Val His Trp Asn Phe Phe Thr Leu Gly Leu Leu Pro Pro Phe Val 245 250 255	879
gag gtc ttc gac gcc ttg gct acg atc att ccg tca tac gag gtt ctc Glu Val Phe Asp Ala Leu Ala Thr Ile Ile Pro Ser Tyr Glu Val Leu 260 265 270 275	927
tcc gtg ggg atc gcc gtc ttg tat caa gtt gcc cta gag tca aca gac Ser Val Gly Ile Ala Val Leu Tyr Gln Val Ala Leu Glu Ser Thr Asp 280 285 290	975
ttg aaa agc tac atc ctc gtc tcc cct cgt ggg cca agc tta ctg tcc Leu Lys Ser Tyr Ile Leu Val Ser Pro Arg Gly Pro Ser Leu Leu Ser 295 300 305	1023
aag aat cgt gaa ggc gtc ttc tcc ttc tca ggt tat ctc gcg att ttt Lys Asn Arg Glu Gly Val Phe Ser Phe Ser Gly Tyr Leu Ala Ile Phe 310 315 320	1071
ctt gct ggt cgt gcg atc ggc att cgg ata atc cct cgc gga act tct Leu Ala Gly Arg Ala Ile Gly Ile Arg Ile Ile Pro Arg Gly Thr Ser 325 330 335	1119
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ggc gtg caa gcg tta gtg tgg acc act ctt ttt gtg ttg aac tcc act Gly Val Gln Ala Leu Val Trp Thr Thr Leu Phe Val Leu Asn Ser Thr 360 365 370	1215
tat gcg atg gga tac gga gct aat atc cct gtc tcc cgc cgc ctc gct Tyr Ala Met Gly Tyr Gly Ala Asn Ile Pro Val Ser Arg Arg Leu Ala 375 380 385	1263
aac atg ccc tat gtc ctt tgg gtt tcg gcg ttc aac acc gcg caa ctg Asn Met Pro Tyr Val Leu Trp Val Ser Ala Phe Asn Thr Ala Gln Leu 390 395 400	1311
ttt gtg ttc tgc ctg atc gaa aca ctc tgc ttt cct gca gtt cat cgg Phe Val Phe Cys Leu Ile Glu Thr Leu Cys Phe Pro Ala Val His Arg 405 410 415	1359
aca acg act caa gag agc gaa tct gag cga gtc gat ttt gct acg agc	1407

Thr	Thr	Thr	Gln	Glu	Ser	Glu	Ser	Glu	Arg	Val	Asp	Phe	Ala	Thr	Ser															
420				425					430					435																
cga atc atg tcg gcc ttc aat aag aac agt ctc gcg atc ttt ctt ttg															1455															
Arg	Ile	Met	Ser	Ala	Phe	Asn	Lys	Asn	Ser	Leu	Ala	Ile	Phe	Leu	Leu															
				440				445				450																		
gcc aat ctt ctg act gga gct gtg aat ctg agc atc tcc aca att gat															1503															
Ala	Asn	Leu	Leu	Thr	Gly	Ala	Val	Asn	Leu	Ser	Ile	Ser	Thr	Ile	Asp															
				455				460			465																			
gct aat aca gca cag gcc atc gct gtt ctc att gga tat tca tcc att															1551															
Ala	Asn	Thr	Ala	Gln	Ala	Ile	Ala	Val	Leu	Ile	Gly	Tyr	Ser	Ser	Ile															
				470				475			480																			
atc aca ggg gtt gct cta gca ttg cat cat gcc aat atc aaa gta ctt															1599															
Ile	Thr	Gly	Val	Ala	Leu	Ala	Leu	His	His	Ala	Asn	Ile	Lys	Val	Leu															
				485				490			495																			
cct ttc tag ggtatttacg agcaatttgtt ggtgtgttga agatatacgt															1648															
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aag tcg gcc aaa gag gcc ttt gtc tcg gat aac cca ggt gct tct atc															103															
Lys	Ser	Ala	Lys	Glu	Ala	Phe	Val	Ser	Asp	Asn	Pro	Gly	Ala	Ser	Ile															
5				10				15			20																			
tgg agt atc aac gct gtc agc ctg gtc gca ctg gtatgttagct cgttctccga															156															
Trp	Ser	Ile	Asn	Ala	Val	Ser	Leu	Val	Ala	Leu																				
				25				30																						
ggggttctgt catttggaga cgcttattaa ttgggatcgc ag gcg aca tat gct															210															
														Ala	Thr	Tyr	Ala													
														35																

ctc tgg atc gcc tta tcg ccg tac atc cgt cat gga ctc ctg aac aac Leu Trp Ile Ala Leu Ser Pro Tyr Ile Arg His Gly Leu Leu Asn Asn 40 45 50	258
tac ctg atc tgt gtt ctt ccc cta tta ttc ggg gtg acc atc ttc tca Tyr Leu Ile Cys Val Leu Pro Leu Leu Phe Gly Val Thr Ile Phe Ser 55 60 65	306
act tcg cct ctc gta ttt acc tct ttt ttg tcc att att tcc ctc gct Thr Ser Pro Leu Val Phe Thr Ser Phe Leu Ser Ile Ile Ser Leu Ala 70 75 80	354
ttc atc acg aaa tcc caa aaa tgc ttc aaa tct gtc agt tcg ccc gaa Phe Ile Thr Lys Ser Gln Lys Cys Phe Lys Ser Val Ser Ser Pro Glu 85 90 95	402
aag cca aaa ggc caa tgg cta gac gaa tca gac tcc gat gag gaa cca Lys Pro Lys Gly Gln Trp Leu Asp Glu Ser Asp Ser Asp Glu Glu Pro 100 105 110 115	450
gcg gaa cct gct tct gca gct gga tct gca gca gtc tca cca gta aag Ala Glu Pro Ala Ser Ala Ala Gly Ser Ala Ala Val Ser Pro Val Lys 120 125 130	498
ctt cta cct tcc caa gtg gcg ttc gct tcc gga tcc cta tta tct ccc Leu Leu Pro Ser Gln Val Ala Phe Ala Ser Gly Ser Leu Leu Ser Pro 135 140 145	546
gat ccg aca aca tcc ccc atg tcg cca agt agt tct tca gct tca gga Asp Pro Thr Thr Ser Pro Met Ser Pro Ser Ser Ser Ala Ser Gly 150 155 160	594
cat gaa gac cct ttg ggg att atg ggc gtt aac aca aga cgg agg tcg cta His Glu Asp Pro Leu Gly Ile Met Gly Val Asn Arg Arg Arg Ser Leu 165 170 175	642
tta gaa gga gtt tcg ctt gat gtt ccg tca cat atc gac tcc aag gtc Leu Glu Gly Val Ser Leu Asp Val Pro Ser His Ile Asp Ser Lys Val 180 185 190 195	690
aga ata tct cct gtt ccc tac ttg agg ctc aaa aag tct agg gca acg Arg Ile Ser Pro Val Pro Tyr Leu Arg Leu Lys Lys Ser Arg Ala Thr 200 205 210	738
aag gcg caa tgg gtg aaa gaa aag gga aga tta cca ttt ttg aca gtg Lys Ala Gln Trp Val Lys Glu Lys Gly Arg Leu Pro Phe Leu Thr Val 215 220 225	786
tac cga gcg cac atg atg ctc atg act gtt atc tgc atc ttg gcg gta Tyr Arg Ala His Met Met Leu Met Thr Val Ile Cys Ile Leu Ala Val 230 235 240	834
gat ttt gaa gtg ttt cct aga tgg cag ggc aag tgc gaa gat ttt ggt Asp Phe Glu Val Phe Pro Arg Trp Gln Gly Lys Cys Glu Asp Phe Gly 245 250 255	882
act agt ctg gtaagcttcc cttcagccat ggtccagtgc tcaccgctct Thr Ser Leu 260	931

acttgccgta g atg gac gtc ggt gtc ggg tca ttc gtc ttt tcc ctc ggt Met Asp Val Gly Val Gly Ser Phe Val Phe Ser Leu Gly 265 270 275	981
ctc gtc tcc aca aaa tct ctt tct cct cca cct cca act cct acg ccc Leu Val Ser Thr Lys Ser Leu Ser Pro Pro Pro Pro Thr Pro Thr Pro 280 285 290	1029
tcc tcg ccc gct ctc aac tct cac atc att ccc ctc acc ccg tcc ccg Ser Ser Pro Ala Leu Asn Ser His Ile Ile Pro Leu Thr Pro Ser Pro 295 300 305	1077
tcc act tcc atc ctc atc tcg ctc cga aaa tcc atc ccc atc ctc gtc Phe Thr Ser Ile Leu Ile Ser Leu Arg Lys Ser Ile Pro Ile Leu Val 310 315 320	1125
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cat gtg acg gag tac ggc gtg cac tgg aat ttc ttc ttc acc ctc gca His Val Thr Glu Tyr Gly Val His Trp Asn Phe Phe Thr Leu Ala 340 345 350 355	1221
ttg gtt cct gtg ctc gcc gtg ggc att cga cca ttg acg cag tgg ctt Leu Val Pro Val Leu Ala Val Gly Ile Arg Pro Leu Thr Gln Trp Leu 360 365 370	1269
cgc tgg agt gtg ctt ggg gta atc atc tct ttg ctg cat cag ctg tgg Arg Trp Ser Val Leu Gly Val Ile Ile Ser Leu Leu His Gln Leu Trp 375 380 385	1317
tta aca tat tat ctc caa tcc atc gtc ttc tca ttc ggc cgg tca ggt Leu Thr Tyr Tyr Leu Gln Ser Ile Val Phe Ser Phe Gly Arg Ser Gly 390 395 400	1365
atc ttt cta gca aac aag gaa ggc ttc tcc tct ctt cct ggt tat ctt Ile Phe Leu Ala Asn Lys Glu Gly Phe Ser Ser Leu Pro Gly Tyr Leu 405 410 415	1413
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agt tta cca cca aga aga gag agg gtc gtg tca gaa aca aat gaa gag Ser Leu Pro Pro Arg Arg Glu Arg Val Val Ser Glu Thr Asn Glu Glu 440 445 450	1509
cat gag cag agt cat ttt gag aga aaa aaa ttg gat ttg att atg gag His Glu Gln Ser His Phe Glu Arg Lys Lys Leu Asp Leu Ile Met Glu 455 460 465	1557
ttg att gga tat agc tta ggc tgg tgg gca ctc tta gga ggc tgg att Leu Ile Gly Tyr Ser Leu Gly Trp Trp Ala Leu Leu Gly Gly Trp Ile 470 475 480	1605
tgg gcc ggc ggg gag gta tcc agg cgt tta gtaagtggac atctttggta Trp Ala Gly Gly Glu Val Ser Arg Arg Leu 485 490	1655
atattgtacc tatactaatac cctgcataaa g gcc aac gct cct tat gta ttt	1707

Ala Asn Ala Pro Tyr Val Phe			
495	500		
tgg gta gcg gca tac aat acc acc ttt ctc ctc ggc tac ctc ctc ctt			1755
Trp Val Ala Ala Tyr Asn Thr Thr Phe Leu Leu Gly Tyr Leu Leu			
505	510	515	
acc cac att att cca tct ccc acc tct tcc caa aca tca cca tcg atc			1803
Thr His Ile Ile Pro Ser Pro Thr Ser Ser Gln Thr Ser Pro Ser Ile			
520	525	530	
tta gtg cct ccc ttg ctc gac gct atg aat aaa aac ggt ctc gcg ata			1851
Leu Val Pro Pro Leu Leu Asp Ala Met Asn Lys Asn Gly Leu Ala Ile			
535	540	545	
ttt ttg gcg gcc aac ttg ctt aca gga ctg gtg aat gtg agc atg aag			1899
Phe Leu Ala Ala Asn Leu Leu Thr Gly Leu Val Asn Val Ser Met Lys			
550	555	560	
aca atg tat gcg ccg gcg tgg ttg tca atg ggg gtg tta atg ttg tat			1947
Thr Met Tyr Ala Pro Ala Trp Leu Ser Met Gly Val Leu Met Leu Tyr			
565	570	575	580
acc ttg aca atc agt tgt gta ggg tgg ata ctg aaa gga cgg agg atc			1995
Thr Leu Thr Ile Ser Cys Val Gly Trp Ile Leu Lys Gly Arg Arg Ile			
585	590	595	
aag ata tagttaaagt gtttaccatg caggatactg agtatctcgg ttca			2045
Lys Ile			

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1	5	10	15

ggt gct tct atc tgg agt atc aac gct gtc agc ctg gtc gca ctg gcg			
Gly Ala Ser Ile Trp Ser Ile Asn Ala Val Ser Leu Val Ala Leu Ala			
20	25	30	

aca tat gct ctc tgg atc gcc tta tcg ccg tac atc cgt cat gga ctc			
Thr Tyr Ala Leu Trp Ile Ala Leu Ser Pro Tyr Ile Arg His Gly Leu			
35	40	45	

ctg aac aac tac ctg atc tgt gtt ctt ccc cta tta ttc ggg gtg acc			
Leu Asn Asn Tyr Leu Ile Cys Val Leu Pro Leu Leu Phe Gly Val Thr			
50	55	60	

atc ttc tca act tcg cct ctc gta ttt acc tct ttt ttg tcc att att			
Ile Phe Ser Thr Ser Pro Leu Val Phe Thr Ser Phe Leu Ser Ile Ile			
65	70	75	80

tcc ctc gct ttc atc acg aaa tcc caa aaa tgc ttc aaa tct gtc agt		288	
Ser Leu Ala Phe Ile Thr Lys Ser Gln Lys Cys Phe Lys Ser Val Ser			
85	90	95	
tcg ccc gaa aag cca aaa ggc caa tgg cta gac gaa tca gac tcc gat		336	
Ser Pro Glu Lys Pro Lys Gly Gln Trp Leu Asp Glu Ser Asp Ser Asp			
100	105	110	
gag gaa cca gcg gaa cct gct tct gca gct gga tct gca gca gtc tca		384	
Glu Glu Pro Ala Glu Pro Ala Ser Ala Ala Gly Ser Ala Ala Val Ser			
115	120	125	
cca gta aag ctt cta cct tcc caa gtg gcg ttc gct tcg gga tcc cta		432	
Pro Val Lys Leu Leu Pro Ser Gln Val Ala Phe Ala Ser Gly Ser Leu			
130	135	140	
tta tct ccc gat ccg aca aca tcc ccc atg tcg cca agt agt tct tca		480	
Leu Ser Pro Asp Pro Thr Ser Pro Met Ser Pro Ser Ser Ser Ser			
145	150	155	160
gct tca gga cat gaa gac cct ttg ggg att atg ggc gtt aac aga cgg		528	
Ala Ser Gly His Glu Asp Pro Leu Gly Ile Met Gly Val Asn Arg Arg			
165	170	175	
agg tcg cta tta gaa gga gtt tcg ctt gat gtt ccg tca cat atc gac		576	
Arg Ser Leu Leu Glu Gly Val Ser Leu Asp Val Pro Ser His Ile Asp			
180	185	190	
tcc aag gtc aga ata tct cct gtt ccc tac ttg agg ctc aaa aag tct		624	
Ser Lys Val Arg Ile Ser Pro Val Pro Tyr Leu Arg Leu Lys Lys Ser			
195	200	205	
agg gca acg aag gcg caa tgg gtg aaa gaa aag gga aga tta cca ttt		672	
Arg Ala Thr Lys Ala Gln Trp Val Lys Glu Lys Gly Arg Leu Pro Phe			
210	215	220	
ttg aca gtg tac cga gcg cac atg atg ctc atg act gtt atc tgc atc		720	
Leu Thr Val Tyr Arg Ala His Met Met Leu Met Thr Val Ile Cys Ile			
225	230	235	240
ttg gcg gta gat ttt gaa gtg ttt cct aga tgg cag ggc aag tgc gaa		768	
Leu Ala Val Asp Phe Glu Val Phe Pro Arg Trp Gln Gly Lys Cys Glu			
245	250	255	
gat ttt ggt act agt ctg atg gac gtg ggt gtc ggg tca ttc gtc ttt		816	
Asp Phe Gly Thr Ser Leu Met Asp Val Gly Val Gly Ser Phe Val Phe			
260	265	270	
tcc ctc ggt ctc gtc tcc aca aaa tct ctt tct cct cca cct cca act		864	
Ser Leu Gly Leu Val Ser Thr Lys Ser Leu Ser Pro Pro Pro Pro Thr			
275	280	285	
cct acg ccc tcc tcg ccc gct ctc aac tct cac atc att ccc ctc acc		912	
Pro Thr Pro Ser Ser Pro Ala Leu Asn Ser His Ile Ile Pro Leu Thr			
290	295	300	
ccg tcc ccg ttc act tcc atc ctc atc tcg ctc cga aaa tcc atc ccc		960	

Pro	Ser	Pro	Phe	Thr	Ser	Ile	Leu	Ile	Ser	Leu	Arg	Lys	Ser	Ile	Pro	
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atc	ctc	gtc	ctc	ggc	ttt	ata	cgg	ttg	att	atg	gtc	aag	gga	tct	gat	1008
Ile	Leu	Val	Leu	Gly	Phe	Ile	Arg	Leu	Ile	Met	Val	Lys	Gly	Ser	Asp	
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																330
																335
tat	cct	gag	cat	gtg	acg	gag	tac	ggc	gtg	cac	tgg	aat	ttc	ttc	ttc	1056
Tyr	Pro	Glu	His	Val	Thr	Glu	Tyr	Gly	Val	His	Trp	Asn	Phe	Phe	Phe	
																340
																345
																350
acc	ctc	gca	ttg	gtt	cct	gtg	ctc	gcc	gtg	ggc	att	cga	cca	ttg	acg	1104
Thr	Leu	Ala	Leu	Val	Pro	Val	Leu	Ala	Val	Gly	Ile	Arg	Pro	Leu	Thr	
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cag	tgg	ctt	cgc	tgg	agt	gtg	ctt	ggg	gta	atc	atc	tct	ttg	ctg	cat	1152
Gln	Trp	Leu	Arg	Trp	Ser	Val	Leu	Gly	Val	Ile	Ser	Leu	Leu	His		
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cag	ctg	tgg	tta	aca	tat	tat	ctc	caa	tcc	atc	gtc	ttc	tca	ttc	ggc	1200
Gln	Leu	Trp	Leu	Thr	Tyr	Tyr	Leu	Gln	Ser	Ile	Val	Phe	Ser	Phe	Gly	
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																395
																400
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Arg	Ser	Gly	Ile	Phe	Leu	Ala	Asn	Lys	Glu	Gly	Phe	Ser	Ser	Leu	Pro	
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																410
																415
ggt	tat	ctt	tcc	ata	ttt	ttg	atc	ggc	ttg	tct	att	gga	gat	cat	gtt	1296
Gly	Tyr	Leu	Ser	Ile	Phe	Leu	Ile	Gly	Leu	Ser	Ile	Gly	Asp	His	Val	
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tta	agg	ctc	agt	tta	cca	cca	aga	aga	aga	agg	gtc	gtg	tca	gaa	aca	1344
Leu	Arg	Leu	Ser	Leu	Pro	Pro	Arg	Arg	Glu	Arg	Val	Val	Val	Ser	Glu	
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aat	gaa	gag	cat	gag	cag	agt	cat	ttt	gag	aga	aaa	aaa	ttg	gat	ttg	1392
Asn	Glu	Glu	His	Glu	Gln	Ser	His	Phe	Glu	Arg	Lys	Lys	Leu	Asp	Leu	
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																455
																460
att	atg	gag	ttg	att	gga	tat	agc	tta	ggc	tgg	tgg	gca	ctc	tta	gga	1440
Ile	Met	Glu	Leu	Ile	Gly	Tyr	Ser	Leu	Gly	Trp	Trp	Ala	Leu	Leu	Gly	
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																470
																475
																480
ggc	tgg	att	tgg	gcc	ggc	ggg	gag	gta	tcc	agg	cgt	tta	gcc	aac	gct	1488
Gly	Trp	Ile	Trp	Ala	Gly	Gly	Glu	Val	Ser	Arg	Arg	Leu	Ala	Asn	Ala	
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																490
																495
cct	tat	gta	ttt	tgg	gta	gcg	gca	tac	aat	acc	acc	ttt	ctc	ctc	ggc	1536
Pro	Tyr	Val	Phe	Trp	Val	Ala	Ala	Tyr	Asn	Thr	Thr	Phe	Leu	Leu	Gly	
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																505
																510
tac	ctc	ctc	ctt	acc	cac	att	att	cca	tct	ccc	acc	tct	tcc	caa	aca	1584
Tyr	Leu	Leu	Thr	His	Ile	Ile	Pro	Ser	Pro	Thr	Ser	Ser	Gln	Thr		
																515
																520
																525
tca	cca	tcg	atc	tta	gtg	cct	ccc	ttg	ctc	gac	gct	atg	aat	aaa	aac	1632
Ser	Pro	Ser	Ile	Leu	Val	Pro	Pro	Leu	Leu	Asp	Ala	Met	Asn	Lys	Asn	
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ggt	ctc	gcg	ata	ttt	ttg	gct	gcc	aac	ttg	ctt	aca	gga	ctg	gtg	aat	1680
Gly	Leu	Ala	Ile	Phe	Leu	Ala	Ala	Asn	Leu	Leu	Thr	Gly	Leu	Val	Asn	

545

550

555

560

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 Val Ser Met Lys Thr Met Tyr Ala Pro Ala Trp Leu Ser Met Gly Val
 565 570 575

tta atg ttg tat acc ttg aca atc agt tgt gta ggg tgg ata ctg aaa 1776
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 580 585 590

gga cgg agg atc aag ata tag 1797
 Gly Arg Arg Ile Lys Ile
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 35 40 45

Leu Asn Asn Tyr Leu Ile Cys Val Leu Pro Leu Leu Phe Gly Val Thr
 50 55 60

Ile Phe Ser Thr Ser Pro Leu Val Phe Thr Ser Phe Leu Ser Ile Ile
 65 70 75 80

Ser Leu Ala Phe Ile Thr Lys Ser Gln Lys Cys Phe Lys Ser Val Ser
 85 90 95

Ser Pro Glu Lys Pro Lys Gly Gln Trp Leu Asp Glu Ser Asp Ser Asp
 100 105 110

Glu Glu Pro Ala Glu Pro Ala Ser Ala Ala Gly Ser Ala Ala Val Ser
 115 120 125

Pro Val Lys Leu Leu Pro Ser Gln Val Ala Phe Ala Ser Gly Ser Leu
 130 135 140

Leu Ser Pro Asp Pro Thr Thr Ser Pro Met Ser Pro Ser Ser Ser Ser
 145 150 155 160

Ala Ser Gly His Glu Asp Pro Leu Gly Ile Met Gly Val Asn Arg Arg
 165 170 175

Arg Ser Leu Leu Glu Gly Val Ser Leu Asp Val Pro Ser His Ile Asp
 180 185 190

Ser Lys Val Arg Ile Ser Pro Val Pro Tyr Leu Arg Leu Lys Lys Ser
 195 200 205

Arg Ala Thr Lys Ala Gln Trp Val Lys Glu Lys Gly Arg Leu Pro Phe

210	215	220																																																																																																																											
Leu Thr Val Tyr Arg Ala His Met Met Leu Met Thr Val Ile Cys Ile																																																																																																																													
225	230	235	240			Leu Ala Val Asp Phe Glu Val Phe Pro Arg Trp Gln Gly Lys Cys Glu			245	250	255	Asp Phe Gly Thr Ser Leu Met Asp Val Gly Val Gly Ser Phe Val Phe			260	265	270	Ser Leu Gly Leu Val Ser Thr Lys Ser Leu Ser Pro Pro Pro Pro Thr			275	280	285	Pro Thr Pro Ser Ser Pro Ala Leu Asn Ser His Ile Ile Pro Leu Thr			290	295	300	Pro Ser Pro Phe Thr Ser Ile Leu Ile Ser Leu Arg Lys Ser Ile Pro			305	310	315	320			Ile Leu Val Leu Gly Phe Ile Arg Leu Ile Met Val Lys Gly Ser Asp			325	330	335	Tyr Pro Glu His Val Thr Glu Tyr Gly Val His Trp Asn Phe Phe Phe			340	345	350	Thr Leu Ala Leu Val Pro Val Leu Ala Val Gly Ile Arg Pro Leu Thr			355	360	365	Gln Trp Leu Arg Trp Ser Val Leu Gly Val Ile Ile Ser Leu Leu His			370	375	380	Gln Leu Trp Leu Thr Tyr Tyr Leu Gln Ser Ile Val Phe Ser Phe Gly			385	390	395	400			Arg Ser Gly Ile Phe Leu Ala Asn Lys Glu Gly Phe Ser Ser Leu Pro			405	410	415	Gly Tyr Leu Ser Ile Phe Leu Ile Gly Leu Ser Ile Gly Asp His Val			420	425	430	Leu Arg Leu Ser Leu Pro Pro Arg Arg Glu Arg Val Val Ser Glu Thr			435	440	445	Asn Glu Glu His Glu Gln Ser His Phe Glu Arg Lys Lys Leu Asp Leu			450	455	460	Ile Met Glu Leu Ile Gly Tyr Ser Leu Gly Trp Trp Ala Leu Leu Gly			465	470	475	480			Gly Trp Ile Trp Ala Gly Gly Glu Val Ser Arg Arg Leu Ala Asn Ala			485	490	495	Pro Tyr Val Phe Trp Val Ala Ala Tyr Asn Thr Thr Phe Leu Leu Gly			500	505	510	Tyr Leu Leu Leu Thr His Ile Ile Pro Ser Pro Thr Ser Ser Gln Thr			515	520	525	Ser Pro Ser Ile Leu Val Pro Pro Leu Leu Asp Ala Met Asn Lys Asn		
240																																																																																																																													
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260	265	270																																																																																																																											
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385	390	395	400			Arg Ser Gly Ile Phe Leu Ala Asn Lys Glu Gly Phe Ser Ser Leu Pro			405	410	415	Gly Tyr Leu Ser Ile Phe Leu Ile Gly Leu Ser Ile Gly Asp His Val			420	425	430	Leu Arg Leu Ser Leu Pro Pro Arg Arg Glu Arg Val Val Ser Glu Thr			435	440	445	Asn Glu Glu His Glu Gln Ser His Phe Glu Arg Lys Lys Leu Asp Leu			450	455	460	Ile Met Glu Leu Ile Gly Tyr Ser Leu Gly Trp Trp Ala Leu Leu Gly			465	470	475	480			Gly Trp Ile Trp Ala Gly Gly Glu Val Ser Arg Arg Leu Ala Asn Ala			485	490	495	Pro Tyr Val Phe Trp Val Ala Ala Tyr Asn Thr Thr Phe Leu Leu Gly			500	505	510	Tyr Leu Leu Leu Thr His Ile Ile Pro Ser Pro Thr Ser Ser Gln Thr			515	520	525	Ser Pro Ser Ile Leu Val Pro Pro Leu Leu Asp Ala Met Asn Lys Asn																																																																				
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465	470	475	480			Gly Trp Ile Trp Ala Gly Gly Glu Val Ser Arg Arg Leu Ala Asn Ala			485	490	495	Pro Tyr Val Phe Trp Val Ala Ala Tyr Asn Thr Thr Phe Leu Leu Gly			500	505	510	Tyr Leu Leu Leu Thr His Ile Ile Pro Ser Pro Thr Ser Ser Gln Thr			515	520	525	Ser Pro Ser Ile Leu Val Pro Pro Leu Leu Asp Ala Met Asn Lys Asn																																																																																																					
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530

535

540

Gly Leu Ala Ile Phe Leu Ala Ala Asn Leu Leu Thr Gly Leu Val Asn
545 550 555 560

Val Ser Met Lys Thr Met Tyr Ala Pro Ala Trp Leu Ser Met Gly Val
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Gly Arg Arg Ile Lys Ile
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<223> Description of Artificial Sequence:an artificially
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35

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synthesized primer sequence

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<211> 60

<212> DNA

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60

<210> 18

<211> 60

<212> DNA

<213> *Saccharomyces cerevisiae*

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